AMENDMENT

1. (Currently Amended) A method for sequencing nucleic acids comprising:

(a) fragmenting large template nucleic acid molecules to generate a plurality of fragmented nucleic acids;

(b) delivering the fragmented nucleic acids into aqueous microreactors in a water-in-oil emulsion such that a plurality of aqueous microreactors comprise a single copy of a fragmented nucleic acid, a single bead capable of binding to the fragmented nucleic acid, and amplification reaction solution containing reagents necessary to perform nucleic acid amplification;

(c) amplifying the fragmented nucleic acids in the microreactors to form amplified copies of said nucleic acids and binding the amplified copies to beads in the microreactors;

(d) delivering the beads to an array of at least 10,000 reaction chambers on a planar surface, wherein a plurality of the reaction chambers comprise no more than a single nucleic acid bound bead; and

(e) performing a sequencing reaction simultaneously on a plurality of the reaction chambers.

2. (Original) The method of claim 1 wherein the reaction chambers have a center to center spacing of 20 to 100 μm.

3. (Original) The method of claim 1 wherein the fragmented nucleic acids are 30 – 500 bases.

4. (Original) The method of claim 1 wherein a plurality of the beads bind at least 10,000 amplified copies.

5. (Original) The method of claim 1 wherein step © is accomplished using polymerase chain reaction.

6. (Original) The method of claim 1 wherein the sequencing reaction is a pyrophosphate-based sequencing reaction.

7. (Original) The method of claim 1 wherein the sequencing reaction comprises the steps of:

(a) annealing an effective amount of a sequencing primer to the amplified copies of the nucleic acid and extending the sequencing primer with a polymerase and a predetermined nucleotide triphosphate to yield a sequencing product and, if the predetermined nucleotide triphosphate is incorporated onto a 3' end of said sequencing primer, a sequencing reaction byproduct; and

(b) identifying the sequencing reaction byproduct, thereby determining the sequence of the nucleic acid in a plurality of the reaction chambers.

8. (Cancelled).

9. (Original) The method of claim 1 wherein the reaction chambers are cavities formed by etching one end of a fiber optic bundle.

10-72. (Cancelled).

73. (Currently Amended) The method of claim 1 further comprising the steps of:

(a) uniquely tagging the fragmented nucleic acids associated with template nucleic acid molecules from different biological sources ~~libraries~~ to create libraries of fragmented nucleic acids with different detectable sequence tags;

(b) sequencing said fragmented nucleic acids and detecting said detectable sequence tag from each said tagged nucleic acid fragment.

74. (Currently Amended) The method of claim ~~1~~ 73 wherein the libraries are delivered to the array of reaction chambers individually or wherein the libraries are mixed and delivered to the array of reaction chambers simultaneously.

75. (Currently Amended) The method of claim ~~1~~ 73 wherein said detectable sequence tag comprises an oligonucleotide of between 2 and 50 bases.

76 to 84. (Cancelled).